

Y. Pak

#6

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/618,623

DATE: 11/27/2001

TIME: 14:02:09

Input Set : A:\15060004.app

Output Set: N:\CRF3\11212001\I618623.raw

ENTERED

3 <110> APPLICANT: GROSS, RICHARD W.  
 4 MANCUSO, DAVID J.  
 6 <120> TITLE OF INVENTION: CALCIUM INDEPENDENT PHOSPHOILPASE A2Y POLYNUCLEOTIDES  
 7 AND POLYPEPTIDES AND METHODS THEREFOR  
 9 <130> FILE REFERENCE: 15060-0004  
 11 <140> CURRENT APPLICATION NUMBER: 09/618,623  
 12 <141> CURRENT FILING DATE: 2000-07-18  
 14 <160> NUMBER OF SEQ ID NOS: 47  
 16 <170> SOFTWARE: PatentIn Ver. 2.1  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 782  
 21 <212> TYPE: PRT  
 22 <213> ORGANISM: Homo sapiens  
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 29 20 25 30  
 31 Phe Ser Pro Lys His Tyr Trp Arg Ile Ser His Ile Ser Leu Gln Arg  
 32 35 40 45  
 34 Gly Phe His Thr Asn Ile Ile Arg Cys Lys Trp Thr Lys Ser Glu Ala  
 35 50 55 60  
 37 His Ser Cys Ser Lys His Cys Tyr Ser Pro Ser Asn His Gly Leu His  
 38 65 70 75 80  
 40 Ile Gly Ile Leu Lys Leu Ser Thr Ser Ala Pro Lys Gly Leu Thr Lys  
 41 85 90 95  
 43 Val Asn Ile Cys Met Ser Arg Ile Lys Ser Thr Leu Asn Ser Val Ser  
 44 100 105 110  
 46 Lys Ala Val Phe Gly Asn Gln Asn Glu Met Ile Ser Arg Leu Ala Gln  
 47 115 120 125  
 49 Phe Lys Pro Ser Ser Gln Ile Leu Arg Lys Val Ser Asp Ser Gly Trp  
 50 130 135 140  
 52 Leu Lys Gln Lys Asn Ile Lys Gln Ala Ile Lys Ser Leu Lys Lys Tyr  
 53 145 150 155 160  
 55 Ser Asp Lys Ser Ala Glu Lys Ser Pro Phe Pro Glu Glu Lys Ser His  
 56 165 170 175  
 58 Ile Ile Asp Lys Glu Glu Asp Ile Gly Lys Arg Ser Leu Phe His Tyr  
 59 180 185 190  
 61 Thr Ser Ser Ile Thr Thr Lys Phe Gly Asp Ser Phe Tyr Phe Leu Ser  
 62 195 200 205  
 64 Asn His Ile Asn Ser Tyr Phe Lys Arg Lys Glu Lys Met Ser Gln Gln  
 65 210 215 220  
 67 Lys Glu Asn Glu His Phe Arg Asp Lys Ser Glu Leu Glu Asp Lys Lys  
 68 225 230 235 240  
 70 Val Glu Glu Gly Lys Leu Arg Ser Pro Asp Pro Gly Ile Leu Ala Tyr  
 71 245 250 255  
 73 Lys Pro Gly Ser Glu Ser Val His Thr Val Asp Lys Pro Thr Ser Pro

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74          260          265          270
76 Ser Ala Ile Pro Asp Val Leu Gln Val Ser Thr Lys Gln Ser Ile Ala
77          275          280          285
79 Asn Phe Leu Ser Arg Pro Thr Glu Gly Val Gln Ala Leu Val Gly Gly
80          290          295          300
82 Tyr Ile Gly Gly Leu Val Pro Lys Leu Lys Tyr Asp Ser Lys Ser Gln
83 305          310          315          320
85 Ser Glu Glu Gln Glu Glu Pro Ala Lys Thr Asp Gln Ala Val Ser Lys
86          325          330          335
88 Asp Arg Asn Ala Glu Glu Lys Lys Arg Leu Ser Leu Gln Arg Glu Lys
89          340          345          350
91 Ile Ile Ala Arg Val Ser Ile Asp Asn Arg Thr Arg Ala Leu Val Gln
92          355          360          365
94 Ala Leu Arg Arg Thr Thr Asp Pro Lys Leu Cys Ile Thr Arg Val Glu
95          370          375          380
97 Glu Leu Thr Phe His Leu Leu Glu Phe Pro Glu Gly Lys Gly Val Ala
98 385          390          395          400
100 Val Lys Glu Arg Ile Ile Pro Tyr Leu Leu Arg Leu Arg Gln Ile Lys
101          405          410          415
103 Asp Glu Thr Leu Gln Ala Ala Val Arg Glu Ile Leu Ala Leu Ile Gly
104          420          425          430
106 Tyr Val Asp Pro Val Lys Gly Arg Gly Ile Arg Ile Leu Ser Ile Asp
107          435          440          445
109 Gly Gly Gly Thr Arg Gly Val Val Ala Leu Gln Thr Leu Arg Lys Leu
110          450          455          460
112 Val Glu Leu Thr Gln Lys Pro Val His Gln Leu Phe Asp Tyr Ile Cys
113 465          470          475          480
115 Gly Val Ser Thr Gly Ala Ile Leu Ala Phe Met Leu Gly Leu Phe His
116          485          490          495
118 Met Pro Leu Asp Glu Cys Glu Glu Leu Tyr Arg Lys Leu Gly Ser Asp
119          500          505          510
121 Val Phe Ser Gln Asn Val Ile Val Gly Thr Val Lys Met Ser Trp Ser
122          515          520          525
124 His Ala Phe Tyr Asp Ser Gln Thr Trp Glu Asn Ile Leu Lys Asp Arg
125          530          535          540
127 Met Gly Ser Ala Leu Met Ile Glu Thr Ala Arg Asn Pro Thr Cys Pro
128 545          550          555          560
130 Lys Val Ala Ala Val Ser Thr Ile Val Asn Arg Gly Ile Thr Pro Lys
131          565          570          575
133 Ala Phe Val Phe Arg Asn Tyr Gly His Phe Pro Gly Ile Asn Ser His
134          580          585          590
136 Tyr Leu Gly Gly Cys Gln Tyr Lys Met Trp Gln Ala Ile Arg Ala Ser
137          595          600          605
139 Ser Ala Ala Pro Gly Tyr Phe Ala Glu Tyr Ala Leu Gly Asn Asp Leu
140          610          615          620
142 His Gln Asp Gly Gly Leu Leu Leu Asn Asn Pro Ser Ala Leu Ala Met
143 625          630          635          640
145 His Glu Cys Lys Cys Leu Trp Pro Asp Val Pro Leu Glu Cys Ile Val
146          645          650          655

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148 Ser Leu Gly Thr Gly Arg Tyr Glu Ser Asp Val Arg Asn Thr Val Thr
149          660          665          670
151 Tyr Thr Ser Leu Lys Thr Lys Leu Ser Asn Val Ile Asn Ser Ala Thr
152          675          680          685
154 Asp Thr Glu Glu Val His Ile Met Leu Asp Gly Leu Leu Pro Pro Asp
155          690          695          700
157 Thr Tyr Phe Arg Phe Asn Pro Val Met Cys Glu Asn Ile Pro Leu Asp
158 705          710          715          720
160 Glu Ser Arg Asn Glu Lys Leu Asp Gln Leu Gln Leu Glu Gly Leu Lys
161          725          730          735
163 Tyr Ile Glu Arg Asn Glu Gln Lys Met Lys Lys Val Ala Lys Ile Leu
164          740          745          750
166 Ser Gln Glu Lys Thr Thr Leu Gln Lys Ile Asn Asp Trp Ile Lys Leu
167          755          760          765
169 Lys Thr Asp Met Tyr Glu Gly Leu Pro Phe Phe Ser Lys Leu
170          770          775          780
173 <210> SEQ ID NO: 2
174 <211> LENGTH: 2349
175 <212> TYPE: DNA
176 <213> ORGANISM: Homo sapiens
178 <220> FEATURE:
179 <221> NAME/KEY: CDS
180 <222> LOCATION: (1)..(2349)
182 <400> SEQUENCE: 2
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184 Met Ser Ile Asn Leu Thr Val Asp Ile Tyr Ile Tyr Leu Leu Ser Asn
185 1 5 10 15
187 gca aga agt gtt tgt ggg aag cag aga agc aag caa ctg tat ttc ttg 96
188 Ala Arg Ser Val Cys Gly Lys Gln Arg Ser Lys Gln Leu Tyr Phe Leu
189 20 25 30
191 ttc tca cct aag cat tac tgg agg ata agc cac atc agt cta caa aga 144
192 Phe Ser Pro Lys His Tyr Trp Arg Ile Ser His Ile Ser Leu Gln Arg
193 35 40 45
195 ggt ttt cat aca aac ata ata aga tgt aaa tgg acc aaa agt gaa gca 192
196 Gly Phe His Thr Asn Ile Ile Arg Cys Lys Trp Thr Lys Ser Glu Ala
197 50 55 60
199 cat tct tgc agt aag cac tgt tac tct cca agc aac cat ggt tta cat 240
200 His Ser Cys Ser Lys His Cys Tyr Ser Pro Ser Asn His Gly Leu His
201 65 70 75 80
203 att ggg att ttg aaa ctt agc act tct gct ccc aag gga ctt aca aaa 288
204 Ile Gly Ile Leu Lys Leu Ser Thr Ser Ala Pro Lys Gly Leu Thr Lys
205 85 90 95
207 gtg aac att tgt atg tcc cgt att aaa agt act ttg aac tct gtt tca 336
208 Val Asn Ile Cys Met Ser Arg Ile Lys Ser Thr Leu Asn Ser Val Ser
209 100 105 110
211 aag gct gtt ttt ggc aat caa aat gaa atg att tca cgt tta gct caa 384
212 Lys Ala Val Phe Gly Asn Gln Asn Glu Met Ile Ser Arg Leu Ala Gln
213 115 120 125
215 ttt aag cca agt tcc caa att tta aga aaa gta tcg gat agt ggc tgg 432

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216	Phe	Lys	Pro	Ser	Ser	Gln	Ile	Leu	Arg	Lys	Val	Ser	Asp	Ser	Gly	Trp	
217		130					135					140					
219	tta	aaa	cag	aaa	aac	atc	aaa	caa	gcc	atc	aaa	tct	ctg	aaa	aaa	tat	480
220	Leu	Lys	Gln	Lys	Asn	Ile	Lys	Gln	Ala	Ile	Lys	Ser	Leu	Lys	Lys	Tyr	
221	145					150					155					160	
223	agt	gac	aaa	tca	gca	gaa	aag	agt	cct	ttt	cca	gaa	gag	aaa	agt	cac	528
224	Ser	Asp	Lys	Ser	Ala	Glu	Lys	Ser	Pro	Phe	Pro	Glu	Glu	Lys	Ser	His	
225					165					170					175		
227	att	ata	gac	aaa	gaa	gaa	gat	ata	ggg	aaa	cgc	agt	ctt	ttt	cat	tac	576
228	Ile	Ile	Asp	Lys	Glu	Glu	Asp	Ile	Gly	Lys	Arg	Ser	Leu	Phe	His	Tyr	
229					180					185					190		
231	aca	agt	tct	ata	acc	aca	aaa	ttt	gga	gac	tca	ttc	tac	ttt	tta	tca	624
232	Thr	Ser	Ser	Ile	Thr	Thr	Lys	Phe	Gly	Asp	Ser	Phe	Tyr	Phe	Leu	Ser	
233			195					200					205				
235	aat	cat	att	aat	tca	tat	ttc	aaa	cgt	aag	gaa	aaa	atg	tct	caa	caa	672
236	Asn	His	Ile	Asn	Ser	Tyr	Phe	Lys	Arg	Lys	Glu	Lys	Met	Ser	Gln	Gln	
237		210					215					220					
239	aag	gaa	aat	gaa	cat	ttc	cgg	gac	aaa	tca	gaa	ctt	gaa	gat	aaa	aag	720
240	Lys	Glu	Asn	Glu	His	Phe	Arg	Asp	Lys	Ser	Glu	Leu	Glu	Asp	Lys	Lys	
241	225					230					235					240	
243	gta	gaa	gag	ggg	aaa	tta	aga	tct	cca	gat	cct	ggc	atc	ctg	gct	tat	768
244	Val	Glu	Glu	Gly	Lys	Leu	Arg	Ser	Pro	Asp	Pro	Gly	Ile	Leu	Ala	Tyr	
245					245					250					255		
247	aag	cca	ggc	tca	gaa	tct	gta	cat	acg	gtg	gac	aag	cct	aca	agt	cct	816
248	Lys	Pro	Gly	Ser	Glu	Ser	Val	His	Thr	Val	Asp	Lys	Pro	Thr	Ser	Pro	
249			260						265					270			
251	tct	gcg	ata	cct	gat	gtt	ctt	caa	gtt	tca	act	aaa	caa	agt	att	gct	864
252	Ser	Ala	Ile	Pro	Asp	Val	Leu	Gln	Val	Ser	Thr	Lys	Gln	Ser	Ile	Ala	
253			275					280					285				
255	aac	ttt	ctt	tct	cgt	ccc	acg	gaa	ggg	gta	caa	gct	tta	gta	ggg	ggg	912
256	Asn	Phe	Leu	Ser	Arg	Pro	Thr	Glu	Gly	Val	Gln	Ala	Leu	Val	Gly	Gly	
257		290					295					300					
259	tat	att	ggg	gga	ctt	gtc	ccc	aaa	tta	aag	tat	gat	tca	aag	agt	cag	960
260	Tyr	Ile	Gly	Gly	Leu	Val	Pro	Lys	Leu	Lys	Tyr	Asp	Ser	Lys	Ser	Gln	
261	305					310					315					320	
263	tca	gaa	gaa	cag	gaa	gag	cct	gct	aaa	act	gat	cag	gct	gtc	agc	aaa	1008
264	Ser	Glu	Glu	Gln	Glu	Glu	Pro	Ala	Lys	Thr	Asp	Gln	Ala	Val	Ser	Lys	
265					325					330					335		
267	gac	aga	aat	gca	gag	gag	aaa	aag	cgt	tta	tct	ctt	cag	cga	gaa	aag	1056
268	Asp	Arg	Asn	Ala	Glu	Glu	Lys	Lys	Arg	Leu	Ser	Leu	Gln	Arg	Glu	Lys	
269				340					345					350			
271	att	atc	gca	agg	gtg	agt	att	gat	aac	agg	acc	cgg	gca	tta	gtt	cag	1104
272	Ile	Ile	Ala	Arg	Val	Ser	Ile	Asp	Asn	Arg	Thr	Arg	Ala	Leu	Val	Gln	
273			355					360					365				
275	gca	tta	aga	aga	aca	act	gac	cca	aag	ctc	tgc	att	act	agg	gtt	gaa	1152
276	Ala	Leu	Arg	Arg	Thr	Thr	Asp	Pro	Lys	Leu	Cys	Ile	Thr	Arg	Val	Glu	
277		370					375					380					
279	gaa	ctg	act	ttt	cat	ctt	cta	gaa	ttt	cct	gaa	gga	aaa	gga	gtg	gct	1200
280	Glu	Leu	Thr	Phe	His	Leu	Leu	Glu	Phe	Pro	Glu	Gly	Lys	Gly	Val	Ala	

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Output Set: N:\CRF3\11212001\I618623.raw

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281 385          390          395          400
283 gtc aag gaa aga att att cca tat tta tta cga ctg aga caa att aag 1248
284 Val Lys Glu Arg Ile Ile Pro Tyr Leu Leu Arg Leu Arg Gln Ile Lys
285          405          410          415
287 gat gaa act ctt cag gct gca gtt aga gaa att ttg gcc cta att ggc 1296
288 Asp Glu Thr Leu Gln Ala Ala Val Arg Glu Ile Leu Ala Leu Ile Gly
289          420          425          430
291 tat gtg gat cca gtg aaa ggg aga gga atc cga att ctc tca att gat 1344
292 Tyr Val Asp Pro Val Lys Gly Arg Gly Ile Arg Ile Leu Ser Ile Asp
293          435          440          445
295 ggt gga gga aca agg ggc gtg gtt gct ctc cag acc cta cga aaa tta 1392
296 Gly Gly Gly Thr Arg Gly Val Val Ala Leu Gln Thr Leu Arg Lys Leu
297          450          455          460
299 gtt gaa ctt act cag aag cca gtt cat cag ctc ttt gat tac att tgt 1440
300 Val Glu Leu Thr Gln Lys Pro Val His Gln Leu Phe Asp Tyr Ile Cys
301 465          470          475          480
303 ggt gta agc aca ggt gcc ata tta gct ttc atg ttg ggg ttg ttt cat 1488
304 Gly Val Ser Thr Gly Ala Ile Leu Ala Phe Met Leu Gly Leu Phe His
305          485          490          495
307 atg ccc ttg gat gaa tgt gag gaa ctt tat cga aaa tta gga tca gat 1536
308 Met Pro Leu Asp Glu Cys Glu Glu Leu Tyr Arg Lys Leu Gly Ser Asp
309          500          505          510
311 gta ttt tca caa aat gtc att gtt gga aca gta aaa atg agt tgg agc 1584
312 Val Phe Ser Gln Asn Val Ile Val Gly Thr Val Lys Met Ser Trp Ser
313          515          520          525
315 cat gca ttt tat gac agt caa aca tgg gaa aac att ctt aag gat agg 1632
316 His Ala Phe Tyr Asp Ser Gln Thr Trp Glu Asn Ile Leu Lys Asp Arg
317          530          535          540
319 atg gga tct gca ctg atg att gaa aca gca aga aac ccc aca tgt cct 1680
320 Met Gly Ser Ala Leu Met Ile Glu Thr Ala Arg Asn Pro Thr Cys Pro
321 545          550          555          560
323 aag gta gct gct gta agt acc ata gta aat aga ggg ata aca ccc aaa 1728
324 Lys Val Ala Ala Val Ser Thr Ile Val Asn Arg Gly Ile Thr Pro Lys
325          565          570          575
327 gct ttt gtg ttc aga aac tat ggt cat ttt cct gga atc aac tct cat 1776
328 Ala Phe Val Phe Arg Asn Tyr Gly His Phe Pro Gly Ile Asn Ser His
329          580          585          590
331 tat ttg gga ggc tgt cag tat aaa atg tgg cag gcc att aga gcc tca 1824
332 Tyr Leu Gly Gly Cys Gln Tyr Lys Met Trp Gln Ala Ile Arg Ala Ser
333          595          600          605
335 tct gct gct cca ggc tac ttt gca gaa tat gca ttg gga aat gat ctt 1872
336 Ser Ala Ala Pro Gly Tyr Phe Ala Glu Tyr Ala Leu Gly Asn Asp Leu
337          610          615          620
339 cat caa gat gga ggt ttg ctt ctg aat aac cct tcg gca tta gct atg 1920
340 His Gln Asp Gly Gly Leu Leu Leu Asn Asn Pro Ser Ala Leu Ala Met
341 625          630          635          640
343 cat gag tgt aaa tgt ctt tgg cca gat gtg ccg tta gag tgc ata gta 1968
344 His Glu Cys Lys Cys Leu Trp Pro Asp Val Pro Leu Glu Cys Ile Val
345          645          650          655

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

**VERIFICATION SUMMARY**

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Input Set : **A:\15060004.app**

Output Set: **N:\CRF3\11212001\I618623.raw**

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L:2054 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36